

SEQUENCE LISTING



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<120> Receptor

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<140> US 10/714,161

<141> 2003-11-14

<150> PCT/GB02/02304

<151> 2002-05-16

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<170> PatentIn Ver. 2.1

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<212> DNA

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 Tyr Leu Ile Ile Phe Val Ala Ser Ile Leu Leu Asn Gly Leu Ala Val
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 Trp Ile Phe Phe His Ile Arg Asn Lys Thr Ser Phe Ile Phe Tyr Leu
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 Lys Asn Ile Val Val Ala Asp Leu Ile Met Thr Leu Thr Phe Pro Phe
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 Arg Ile Val His Asp Ala Gly Phe Gly Pro Trp Tyr Phe Lys Phe Ile
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Leu Cys Arg Tyr Thr Ser Val Leu Phe Tyr Ala Asn Met Tyr Thr Ser
115 120 125

Ile Val Phe Leu Gly Leu Ile Ser Ile Asp Arg Tyr Leu Lys Val Val
130 135 140

Lys Pro Phe Gly Asp Ser Arg Met Tyr Ser Ile Thr Phe Thr Lys Val
145 150 155 160

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Ser Lys Leu Lys Ser Pro Leu Gly Val Lys Trp His Thr Ala Val Thr
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Tyr Val Asn Ser Cys Leu Phe Val Ala Val Leu Val Ile Leu Ile Gly
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Cys Tyr Ile Ala Ile Ser Arg Tyr Ile His Lys Ser Ser Arg Gln Phe
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Ile Ser Gln Ser Ser Arg Lys Arg Lys His Asn Gln Ser Ile Arg Val
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Val Val Ala Val Phe Phe Thr Cys Phe Leu Pro Tyr His Leu Cys Arg
260 265 270

Ile Pro Phe Thr Phe Ser His Leu Asp Arg Leu Leu Asp Glu Ser Ala
275 280 285

Gln Lys Ile Leu Tyr Tyr Cys Lys Glu Ile Thr Leu Phe Leu Ser Ala
290 295 300

Cys Asn Val Cys Leu Asp Pro Ile Ile Tyr Phe Phe Met Cys Arg Ser
305 310 315 320

Phe Ser Arg Arg Leu Phe Lys Lys Ser Asn Ile Arg Thr Arg Ser Glu
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340 345 350

Tyr Asp Tyr Thr Asp Val
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<213> Mus musculus

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<212> PRT

<213> Mus musculus

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Asn Ser Thr Leu His Asn Lys Phe Asp Thr Ile Ile Leu Pro Val Leu
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Tyr Leu Val Ile Phe Val Ala Ser Ile Leu Leu Asn Gly Leu Ala Val
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Trp Ile Phe Phe His Ile Arg Asn Lys Thr Ser Phe Ile Phe Tyr Leu
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Lys Asn Ile Val Val Ala Asp Leu Ile Met Thr Leu Thr Phe Pro Phe
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Met Lys Leu Lys Ser Pro Leu Gly Ala Lys Trp His Met Ala Val Thr
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Tyr Val Asp Ser Cys Leu Phe Val Ala Val Leu Val Ile Leu Ile Gly
210 215 220

Cys Tyr Ile Ala Ile Ser Arg Tyr Ile His Lys Ser Ser Arg Gln Phe
225 230 235 240

Ile Ser Gln Ser Ser Arg Lys Arg Lys His Asn Gln Ser Ile Arg Val
245 250 255

Val Val Ala Val Phe Phe Thr Cys Phe Leu Pro Tyr His Leu Cys Arg
260 265 270

Ile Pro Phe Thr Phe Ser Asn Leu Asp Arg Leu Leu Asp Glu Ser Ala
275 280 285

His Lys Ile Leu Tyr Tyr Cys Lys Glu Met Thr Leu Phe Leu Ser Ala
290 295 300

Cys Asn Val Cys Leu Asp Pro Ile Ile Tyr Phe Phe Met Cys Lys Ser
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Phe Ser Arg Arg Leu Phe Lys Lys Ser Asn Ile Arg Thr Arg Ser Glu
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Tyr Asp Tyr Thr Asp Val
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<210> 6

<211> 384

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Fusion protein
of human Mowgli (SEQ ID NO: 3) with V5 and His
tags at C-terminal end

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50	55	60
Trp Ile Phe Phe His Ile Arg Asn Lys Thr Ser Phe Ile Phe Tyr Leu		
65	70	75 80
Lys Asn Ile Val Val Ala Asp Leu Ile Met Thr Leu Thr Phe Pro Phe		
	85	90 95
Arg Ile Val His Asp Ala Gly Phe Gly Pro Trp Tyr Phe Lys Phe Ile		
	100	105 110
Leu Cys Arg Tyr Thr Ser Val Leu Phe Tyr Ala Asn Met Tyr Thr Ser		
	115	120 125
Ile Val Phe Leu Gly Leu Ile Ser Ile Asp Arg Tyr Leu Lys Val Val		
	130	135 140
Lys Pro Phe Gly Asp Ser Arg Met Tyr Ser Ile Thr Phe Thr Lys Val		
	145	150 155 160
Leu Ser Val Cys Val Trp Val Ile Met Ala Val Leu Ser Leu Pro Asn		
	165	170 175
Ile Ile Leu Thr Asn Gly Gln Pro Thr Glu Asp Asn Ile His Asp Cys		
	180	185 190
Ser Lys Leu Lys Ser Pro Leu Gly Val Lys Trp His Thr Ala Val Thr		
	195	200 205
Tyr Val Asn Ser Cys Leu Phe Val Ala Val Leu Val Ile Leu Ile Gly		
	210	215 220
Cys Tyr Ile Ala Ile Ser Arg Tyr Ile His Lys Ser Ser Arg Gln Phe		
	225	230 235 240
Ile Ser Gln Ser Ser Arg Lys Arg Lys His Asn Gln Ser Ile Arg Val		
	245	250 255
Val Val Ala Val Phe Phe Thr Cys Phe Leu Pro Tyr His Leu Cys Arg		
	260	265 270
Ile Pro Phe Thr Phe Ser His Leu Asp Arg Leu Leu Asp Glu Ser Ala		
	275	280 285
Gln Lys Ile Leu Tyr Tyr Cys Lys Glu Ile Thr Leu Phe Leu Ser Ala		
	290	295 300
Cys Asn Val Cys Leu Asp Pro Ile Ile Tyr Phe Phe Met Cys Arg Ser		
	305	310 315 320
Phe Ser Arg Arg Leu Phe Lys Lys Ser Asn Ile Arg Thr Arg Ser Glu		
	325	330 335
Ser Ile Arg Ser Leu Gln Ser Val Arg Arg Ser Glu Val Arg Ile Tyr		

340

345

350

Tyr Asp Tyr Thr Asp Val Arg Ala Ile Arg Glu Leu Gly Lys Pro Ile
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Pro Asn Pro Leu Leu Gly Leu Asp Ser Ser His His His His His His
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<210> 7

<211> 1104

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Sequence
 comprising Mowgli with NheI and HindIII at the
 5-prime and 3-prime ends

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<210> 8

<211> 366

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Mowgli fusion
 protein comprising a C terminal FLAG tag.

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Asn	Thr	Thr	Leu	His	Asn	Glu	Phe	Asp	Thr	Ile	Val	Leu	Pro	Val	Leu	
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Tyr	Leu	Ile	Ile	Phe	Val	Ala	Ser	Ile	Leu	Leu	Asn	Gly	Leu	Ala	Val	
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Trp	Ile	Phe	Phe	His	Ile	Arg	Asn	Lys	Thr	Ser	Phe	Ile	Phe	Tyr	Leu	
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Lys	Asn	Ile	Val	Val	Ala	Asp	Leu	Ile	Met	Thr	Leu	Thr	Phe	Pro	Phe	
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	290					295					300					
Cys	Asn	Val	Cys	Leu	Asp	Pro	Ile	Ile	Tyr	Phe	Phe	Met	Cys	Arg	Ser	
305					310					315					320	

Phe Ser Arg Arg Leu Phe Lys Lys Ser Asn Ile Arg Thr Arg Ser Glu
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Ser Ile Arg Ser Leu Gln Ser Val Arg Arg Ser Glu Val Arg Ile Tyr
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Tyr Asp Tyr Thr Asp Val Asp Tyr Lys Asp Asp Asp Asp Lys
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<212> DNA

<213> Mus musculus

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<221> CDS

<222> (3984)..(5024)

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<211> 259

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Consensus

<400> 13

Gly	Asn	Leu	Leu	Val	Ile	Leu	Val	Ile	Leu	Arg	Thr	Lys	Lys	Leu	Arg
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Thr	Pro	Thr	Asn	Ile	Phe	Ile	Leu	Asn	Leu	Ala	Val	Ala	Asp	Leu	Leu
			20					25					30		

Phe	Leu	Leu	Thr	Leu	Pro	Pro	Trp	Ala	Leu	Tyr	Tyr	Leu	Val	Gly	Gly
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

35

40

45

Ser Glu Asp Trp Pro Phe Gly Ser Ala Leu Cys Lys Leu Val Thr Ala
50 55 60

Leu Asp Val Val Asn Met Tyr Ala Ser Ile Leu Leu Leu Thr Ala Ile
65 70 75 80

Ser Ile Asp Arg Tyr Leu Ala Ile Val His Pro Leu Arg Tyr Arg Arg
85 90 95

Arg Arg Thr Ser Pro Arg Arg Ala Lys Val Val Ile Leu Leu Val Trp
100 105 110

Val Leu Ala Leu Leu Leu Ser Leu Pro Pro Leu Leu Phe Ser Trp Val
115 120 125

Lys Thr Val Glu Glu Gly Asn Gly Thr Leu Asn Val Asn Val Thr Val
130 135 140

Cys Leu Ile Asp Phe Pro Glu Glu Ser Thr Ala Ser Val Ser Thr Trp
145 150 155 160

Leu Arg Ser Tyr Val Leu Leu Ser Thr Leu Val Gly Phe Leu Leu Pro
165 170 175

Leu Leu Val Ile Leu Val Cys Tyr Thr Arg Ile Leu Arg Thr Leu Arg
180 185 190

Lys Ala Ala Lys Thr Leu Leu Val Val Val Val Val Phe Val Leu Cys
195 200 205

Trp Leu Pro Tyr Phe Ile Val Leu Leu Leu Asp Thr Leu Cys Leu Ser
210 215 220

Ile Ile Met Ser Ser Thr Cys Glu Leu Glu Arg Val Leu Pro Thr Ala
225 230 235 240

Leu Leu Val Thr Leu Trp Leu Ala Tyr Val Asn Ser Cys Leu Asn Pro
245 250 255

Ile Ile Tyr

<210> 14

<211> 256

<212> PRT

<213> Homo sapiens

<400> 14

Leu Asn Gly Leu Ala Val Trp Ile Phe Phe His Ile Arg Asn Lys Thr
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Ser Phe Ile Phe Tyr Leu Lys Asn Ile Val Val Ala Asp Leu Ile Met
20 25 30

Thr Leu Thr Phe Pro Phe Arg Ile Val His Asp Ala Gly Phe Gly Pro
 35 40 45
 Trp Tyr Phe Lys Phe Ile Leu Cys Arg Tyr Thr Ser Val Leu Phe Tyr
 50 55 60
 Ala Asn Met Tyr Thr Ser Ile Val Phe Leu Gly Leu Ile Ser Ile Asp
 65 70 75 80
 Arg Tyr Leu Lys Val Val Lys Pro Phe Gly Asp Ser Arg Met Tyr Ser
 85 90 95
 Ile Thr Phe Thr Lys Val Leu Ser Val Cys Val Trp Val Ile Met Ala
 100 105 110
 Val Leu Ser Leu Pro Asn Ile Ile Leu Thr Asn Gly Gln Pro Thr Glu
 115 120 125
 Asp Asn Ile His Asp Cys Ser Lys Leu Lys Ser Pro Leu Gly Val Lys
 130 135 140
 Trp His Thr Ala Val Thr Tyr Val Asn Ser Cys Leu Phe Val Ala Val
 145 150 155 160
 Leu Val Ile Leu Ile Gly Cys Tyr Ile Ala Ile Ser Arg Tyr Ile His
 165 170 175
 Lys Ser Ser Arg Gln Phe Ile Ser Gln Ser Ser Arg Lys Arg Lys His
 180 185 190
 Asn Gln Ser Ile Arg Val Val Val Ala Val Phe Phe Thr Cys Phe Leu
 195 200 205
 Pro Tyr His Leu Cys Arg Ile Pro Phe Thr Phe Ser His Leu Asp Arg
 210 215 220
 Leu Leu Asp Glu Ser Ala Gln Lys Ile Leu Tyr Tyr Cys Lys Glu Ile
 225 230 235 240
 Thr Leu Phe Leu Ser Ala Cys Asn Val Cys Leu Asp Pro Ile Ile Tyr
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<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 15

actccatctg gtaggtagg cagtgc

<210> 16
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 16
ataccatggt gcctggtcca gatagac

27

<210> 17
<211> 37
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

<400> 17
aaagcgccgc cgtatgtggc catcaagaaa cgtgaac

37

<210> 18
<211> 35
<212> DNA
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<223> Description of Artificial Sequence: Primer

<400> 18
tttactagtt ctcccatgt ccctcacttg tgctg

35

<210> 19
<211> 38
<212> DNA
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<223> Description of Artificial Sequence: Primer

<400> 19
aaaggcgcgc caacacctgc acctgcctcc tggaactc

38

<210> 20
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 20
aaaggccggc cacagcacac tgatcacagc atcatc

36

<210> 21
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 21
gatagcaca gtgccaccct gtgatag

27

<210> 22
<211> 27
<212> DNA
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<400> 22
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27

<210> 23
<211> 27
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<400> 23
gtcttctcta ggcactgtgt ttgaagc

27

<210> 24
<211> 27
<212> DNA
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<220>
<223> Description of Artificial Sequence: Primer

<400> 24
ttggctgaag cccatcaaaa acacaag

27

<210> 25
<211> 27
<212> DNA
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<220>
<223> Description of Artificial Sequence: Primer

<400> 25
gtgagttcca ggaggcaggt gcaggtg

27

<210> 26
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 26
ctgcttcctc ccgtatcact tgtg

24

<210> 27
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 27
gctttcgctc ctggttctta tgtttg

26

<210> 28
<211> 27
<212> DNA
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<220>
<223> Description of Artificial Sequence: Primer

<400> 28
cagccgaact gttcgccagg ctcaagg

27

<210> 29
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 29
cgcacgcct tctatcgcct tcttgac

27

<210> 30
<211> 34

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

<400> 30

taatatgcta gcagaatggg gttcaacttg acgc

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<210> 31

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 31

cgcataatatt atgattacac tgatgtgtag aagcttttta ta

42

<210> 32

<211> 66

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 32

tataaaaagc ttctacttat cgtcgcatc cttgtaatcc acatcagtg aatcataata 60
tatgcg 66